Table S1. Oligonucleotide primer sequences and polymerase chain reaction conditions.

Gene	Chromosome	Variant(s)	NUC or position	Forward primer	Reverse Primer	Length (bp)	Technique	Seq Primer	Tm (°C)
ACE2	Xp22.2	rs2285666	c.439+4G>A	GCATTCTCTTCAGCAAAATTTCCA	[BIO]GTGTTGAAACACACATATCTGCAA	237	Pyrosequencing	ATTACTTGAACCAGGTA	60
ACE2	Xp22.2	several*	X:15600634-15601127	ATCTGTCCTCTCCAGGATGAAC	TCAGTTTCACGGGCAGTAATC	449	Sanger sequencing	-	60
ACE	17q23.3	rs4344†	c.584-105_584-104ins	[BIO]GACTGAGAGACTCCAGCCCT	CACTCACAGCCTCTTCCTCG	223	Pyrosequencing	TTATTAACTTCTTCCCC	65

Abbreviations: NUC = nucleotide change; [BIO] = biotinylated primer; Seq = Pyrosequencing primer; Tm = annealing temperature.

*Multiple target SNPs with a minor allele frequency of at least 0.005 in the European population were analysed by Sanger sequencing in the gene *ACE2* (see Supplementary Table S2).

†rs4344 which is in complete linkage disequilibrium (r^2 = 1.0, D‘ = 1.0) with rs1799752 (D/I) was genotyped as a surrogate SNP.

Table S2. Single nucleotide polymorphisms located within the analyzed *ACE2* coding region.

Variant	Chromosomal location	Minor allele frequency (European), gnomAD database	Amino acid change
rs73635825	X:15600857	0.000	S19P
rs1244687367	X:15600850	0.000	I21T
rs778030746	X:15600851	< 0.001	I21V
rs756231991	X:15600845	< 0.001	E23K
rs1434130600	X:15600839	0.000	A25T
rs1299103394	X:15600836	< 0.001	K26E
rs4646116	X:15600835	0.006	K26R
rs781255386	X:15600833	0.000	T27A
rs1348114695	X:15600809	< 0.001	E35K
rs778500138	X:15600807	0.000	E35D
rs146676783	X:15600803	0.000	E37K
rs1447927937	X:15600783	0.000	S43R
rs1192192618	X:15600763	< 0.001	Y50F
rs760159085	X:15600761	0.000	N51D
rs1569243690	X:15600760	< 0.001	N51S
rs1325542104	X:15600728	0.000	M62V

This table includes the most discussed single nucleotide polymorphisms located in the coding region of *ACE2* with a potential influence on SARS-CoV-2 binding affinity of the viral spike (S) protein to the human ACE2. Sanger sequencing was performed for the complete sequence coding for amino acids 1-62, in which variants with the highest minor allele frequencies in the European population are located. Additional observed variants (not reported in this table), with unknown functional impact, will be reported in the result section.